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☐ 1: Q13268. Dehydrogenase/red...[gi:3915733]

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LOCUS Q13268 258 aa linear PRI 15-SEP-2003
 DEFINITION Dehydrogenase/reductase SDR family member 2 (HEP27 protein)
 (Protein D).
 ACCESSION Q13268
 VERSION Q13268 GI:3915733
 DBSOURCE swissprot: locus DHS2_HUMAN, accession Q13268;
 class: standard.
 extra accessions:Q9H2R2,created: Nov 1, 1997.
 sequence updated: Dec 15, 1998.
 annotation updated: Sep 15, 2003.
 xrefs: gi: [1079565](#), gi: [1079566](#), gi: [11275674](#), gi: [11275675](#), gi:
[13938401](#), gi: [13938402](#)
 xrefs (non-sequence databases): HSSPP50162, GenewHGNC:18349,
 GOGO:0005634, GOGO:0004022, GOGO:0005489, GOGO:0005975,
 InterProIPR002198, PfamPF00106, PRINTSPR00080, PROSITEPS00061
 KEYWORDS Oxidoreductase; Nuclear protein.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 258)
 AUTHORS Gabrielli,F., Donadel,G., Bensi,G., Heguy,A. and Melli,M.
 TITLE A nuclear protein, synthesized in growth-arrested human
 hepatoblastoma cells, is a novel member of the short-chain alcohol
 dehydrogenase family
 JOURNAL Eur. J. Biochem. 232 (2), 473-477 (1995)
 MEDLINE [96035881](#)
 PUBMED [7556196](#)
 REMARK SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
 REFERENCE 2 (residues 1 to 258)
 AUTHORS Pellegrini,S., Censini,S., Guidotti,S., Covacci,A. and Gabrielli,F.
 TITLE Direct Submission
 JOURNAL Submitted (~MAR-2000)
 REMARK SEQUENCE FROM N.A.
 REFERENCE 3 (residues 1 to 258)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S.N., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J.M. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE [22388257](#)

PUBMED [12477932](#)

REMARK SEQUENCE FROM N.A.
 TISSUE=Skin

REFERENCE 4 (residues 1 to 258)

AUTHORS Donadel,G., Garzelli,C., Frank,R. and Gabrielli,F.

TITLE Identification of a novel nuclear protein synthesized in
 growth-arrested human hepatoblastoma HepG2 cells

JOURNAL Eur. J. Biochem. 195 (3), 723-729 (1991)

MEDLINE [91153312](#)

PUBMED [1847869](#)

REMARK SEQUENCE OF 57-65; 118-123; 125-139 AND 175-182.

COMMENT On Nov 23, 1998 this sequence version replaced gi:[2492750](#).

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 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[FUNCTION] May inhibit cell replication either by catalyzing the
 oxidation of estrogen and androgen or by converting cortisone in
 cortisol.
 [SUBCELLULAR LOCATION] Nuclear.
 [SIMILARITY] Belongs to the short-chain dehydrogenases/reductases
 (SDR) family.

FEATURES Location/Qualifiers

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gene 1..258
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 /product="Dehydrogenase/reductase SDR family member 2"
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Region 58
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 /region_name="Conflict"
 /note="L -> V (IN REF. 4)."

Region 63
 /gene="DHRS2"
 /region_name="Conflict"
 /note="L -> G (IN REF. 4)."

Site 163
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 /site_type="active"
 /note="BY SIMILARITY."

ORIGIN

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121 svnvkspall lsqllpymen rrgavilvss iaaynpvval gvynvsktal lgltrtlale
181 lapkdirvnc vvpgiiktdf skvfhgnesl wknfkehhl qrigesedca givsflcspd
241 asyvngenia vagystrl
```

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Dec 1 2003 12:53:28

RESULT 1

DHS2_HUMAN

ID DHS2_HUMAN STANDARD; PRT; 257 AA.
 AC Q13268; Q9H2R2;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dehydrogenase/reductase SDR family member 2 (HEP27 protein) (Protein
 DE D).
 GN DHRS2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
 RX MEDLINE=96035881; PubMed=7556196;
 RA Gabrielli F., Donadel G., Bensi G., Heguy A., Melli M.;
 RT "A nuclear protein, synthesized in growth-arrested human
 RT hepatoblastoma cells, is a novel member of the short-chain alcohol
 RT dehydrogenase family.";
 RL Eur. J. Biochem. 232:473-477(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pellegrini S., Censini S., Guidotti S., Covacci A., Gabrielli F.;
 RT "Human Hep27 chromosomal gene.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 57-65; 118-123; 125-139 AND 175-182.
 RX MEDLINE=91153312; PubMed=1847869;
 RA Donadel G., Garzelli C., Frank R., Gabrielli F.;
 RT "Identification of a novel nuclear protein synthesized in growth-
 RT arrested human hepatoblastoma HepG2 cells.";

SCRM-1

RL Eur. J. Biochem. 195:723-729(1991).
 CC -!- FUNCTION: May inhibit cell replication either by catalyzing the
 CC oxidation of estrogen and androgen or by converting cortisone in
 CC cortisol.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC -----
 DR EMBL; U31875; AAA82048.1; ALT_INIT.
 DR EMBL; AF244132; AAG33703.1; ALT_INIT.
 DR EMBL; BC007339; AAH07339.1; -.
 DR HSSP; P50162; 1AE1.
 DR Genew; HGNC:18349; DHRS2.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0004022; F:alcohol dehydrogenase activity; TAS.
 DR GO; GO:0005489; F:electron transporter activity; TAS.
 DR GO; GO:0005975; P:carbohydrate metabolism; TAS.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; Nuclear protein.
 FT INIT_MET 0 0
 FT NP_BIND 17 41 NAD OR NADP (BY SIMILARITY).
 FT ACT_SITE 162 162 BY SIMILARITY.
 FT CONFLICT 57 57 L -> V (IN REF. 4).
 FT CONFLICT 62 62 L -> G (IN REF. 4).
 SQ SEQUENCE 257 AA; 27307 MW; 612298E883725CAC CRC64;

Query Match 55.3%; Score 773.5; DB 1; Length 257;
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 QY 80 GLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFGSIMDVTEEVWDKTLTD 139
 Db 61 GLSVAGIVCHVGKAEDREQLVAKALEHCGGVDFLVCSAGVNPLVGSTLGTSEQIWDKILS 120
 QY 140 INVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSYVNVSKTALLGLNNTLAIE 199
 Db 121 VNVKSPALLLSQLLPYEMENR-RGAVILVSSIAAYNPVVALGVYVNVSKTALLGLTRTLALE 179
 QY 200 LAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDCAGIVSFLCSED 259
 Db 180 LAPKDIRVNCVVPGLIKTDFSKVFGHNSLWKNFKEHHQLQRIGESDCAGIVSFLCSPD 239

Qy 260 ASYITGETVVVG 272
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Db 240 ASYVNGENIAVAG 252